

**Comparative RNA-seq analysis of resistant and susceptible banana genotypes reveals molecular mechanisms in response to *Banana bunchy top virus* (BBTV) infection**

Darlon V. Lantican, Jen Daine L. Nocum, Anand Noel C. Manohar, Jay-Vee S. Mendoza, Roanne R. Gardoce, Grace C. Lachica, Lavernee S. Gueco and Fe M. Dela Cueva

Supplementary Table S4. Validation of differentially expressed genes with RT-qPCR and concordance to RNA-seq analysis.

GENE ID	GENE FUNCTION	Forward Sequence	Reverse Sequence	RNA-Seq fold change	qPCR validation fold change	Concordant? (yes/no)
Ma07_g10990	<i>Adagio-like protein</i>	TCGAGAACGCCACCGGATAC	AGCGGAGTGCCATCCTTCTA	5.302083346	30.31	yes
Ma06_g31610	<i>Probable zinc metalloprotease EGY1</i>	ACGAGGACCTGAACTCGGA	TCCAAGCAGTTCCAGAAGCT	1.661500848	4.52	yes
Ma10_g05760	<i>Nematode resistance protein-like HSPRO2</i>	AGACTTCTGGCAGACCGAT	AACGCTTGTCAGTGCCACT	-2.854365873	2.107297177	no
Ma07_g23140	<i>protein detoxification</i>	CTGAGGTTGCCATAGATGC	CCTGCTGCTGACAAGAAAC	-2.973160419	0.715247784	yes
Ma07_g26720	<i>leucine rich repeat protein kinase VI</i>	GCTTGAAGCTGCTTGTGAGG	TCGGTAGATGTGATGGTGGTCG	-2.40301635	4.729922787	no
Ma06_g30390	<i>light regulated protein</i>	ATCGCGCCCAGGTCATCCAA	ACGCCTCTCCACCAACTACA	3.446473912	3.628448845	yes
Ma03_g28040	<i>chitinase</i>	GCAGACCTCTCATGAAACC	CTATAGCTTTCCAGCTTGG	-3.731093357	0.876714068	yes
Ma08_g29650	<i>Glucuronoxylan 4-O-methyltransferase</i>	CCATCGTCCACTACACCACC	GCCGAAGACCAGGAAGTTGC	3.722648648	14.28070438	yes
Ma11_g13780	<i>BTB domain-containing protein</i>	CATCCTCCAATCCCTCCAAG	CTCAGCTCCGTGTATACTTTC	2.36212275	4.16334547	yes
Ma02_g14310	<i>EDR2_C domain-containing protein</i>	CGTCCTCAGCATGATTTTC	CAGCTTCAGCCTGTCAAG	-3.194588833	1.791539176	no
Ma08_g06150	<i>alkaline/neutral invertase</i>	CTAGTCACTGATGGCTCTTGC	CAGTCTGTTATTGATAGCACGC	3.896274205	3.115384629	yes
Ma11_g20430	<i>RuBisCO</i>	CAATGCTGTCGGTGTTAC	GCACGAGCAATAGTTACC	1.618934505	5.879492288	yes
Ma11_g09120	<i>Eukaryotic translation initiation factor 5A-5</i>	GGTACATCGTCATCAAGAACAG	GAAGATGGCACAATATCCTCAAG	2.609649947	2.190776629	yes
Ma06_g32730	<i>J domain-containing protein</i>	GAAACCCAATGAGAACAGCCAAG	CGATGAAGTCCAGCAATCTTG	2.933901567	2.024284925	yes
Ma03_g29390	<i>HATPase C domain-containing protein</i>	CCTGGAGATACGGATCAAGC	GAACCTTGACGTACCACTCTG	3.268812451	6.549655028	yes
Ma03_g29391	<i>APETALA-like 2</i>	CAATGGAAGGGAGGCAGTC	GGACTATGAACATCAGGTTG	-1.884064013	4.071357462	no
internal control gene	<i>L2</i>	AGGGTTCATAGCCACACCAC	CCGAACTGAGAAGCCCCTAC			

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